

Db 876 GAGATGAGACCATGAGATCAATACCAAGACACATCAAGGCTCTGTGTGAC 935  
 QY 301 \*\*\*PheSerAlaGly\*\*\*AspSerThrAla\*\*\*\*\*ThrGluTrpAlaLeuAlaGluLeu 320  
 Db 936 TTTTCTCGACGAGACACAGATCTCAAGAGGTGACAGAGGAGGACATTCGCAAGATC 995  
 QY 321 IleAsnAsnPro\*\*\*ValLeu\*\*\*\*\*AlaArgGluGlu\*\*\*TyrSerValValGlyLeu 340  
 Db 996 ATCAACATCTCTAGAGTGTGAAAAGGCTCTGAGAGGCTTACAGAGTGTGAGAGAG 1055  
 QY 341 Asp\*\*\*LeuValAspGluValAspTrpGlnAsnLeuProTyrIleArgAlaIleValLeu 360  
 Db 1056 GACACACTGTGAGACGAGATTTGACATCAAACTCTTACATTAGACATGTGAGAG 1115  
 QY 361 GluTrpPheArgMetHisAspProLeuProValValIysArgIysCys\*\*GluGluCys 380  
 Db 1116 GAGACATTCGACATGACCCGCCCTCCAGTGTCAAAAGAGAGACAGAGAGTGT 1175  
 QY 381 \*\*\*IleAsnGly\*\*\*Val\*\*\*ProGluGlyAlaLeu\*\*\*\*\*PheAsnValTrpGlnVal 400  
 Db 1176 GAGATTATGATATGTATGTATCCACAGAGGAGCATGTCTCTTCATATGTATGCAAGTA 1235  
 QY 401 Gly\*\*\*Asp\*\*\*LysTrpTrpAspArgProSerGlu\*\*\*ArgProGluArgPheLeuGlu 420  
 Db 1236 GAGAGAGACCCCAATACCTGGAGACAGCATGAGTTCGCTCTGAGAGGTTCTTAGAG 1295  
 QY 421 Thr\*\*\*AlaGluGlyGluAla\*\*\*\*\*LeuAspLeuArgGly\*\*\*HisPheGlnLeuLeu 440  
 Db 1296 ACAGGAGGTGAGAGGAGAGAGAGGAGGCTCTTATCTTAGGAGACACATTTTCAACTTCTC 1355  
 QY 441 ProPheGlySerGlyArg\*\*\*MetCysProGlyVal\*\*\*LeuAlaThrSerGly\*\*\*Ala 460  
 Db 1356 CCATTGGGTCTGAGAGAGAGAGATGTCCCTGAGATCTGCTTACCTTCCGAGATGAGCA 1415  
 QY 461 ThrLeuLeuAlaSerLeuIleGluCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480  
 Db 1416 ACACCTCTGATCTCTTATTCAGATGCTTGCATTCGAGATGCTGAGTCCACAGAGACAG 1475  
 QY 481 IleLeuIysGly\*\*\*AspAlaIysValSerMetGluGluArgAlaGlyLeuThrValPro 500  
 Db 1476 ATTTTGAAGGCTGTGACGCCCAAGTTAGCATGAGAGAGAGGAGGCTTCACTGTTCCA 1535  
 QY 501 ArgAlaHisSerLeuValCysValProLeuAlaArgGlyValAlaSerIysLeuLeu 520  
 Db 1536 AGGGACATGATCTGTGTCTGTTCATCTTGAAGATGGGAGTTCATTAACCTCTT 1595  
 QY 521 Ser 521  
 Db 1596 TCT 1598  
 RESULT 10  
 AAX60779  
 ID AAX60779 standard; cDNA; 1824 BP.  
 XX  
 AC AAX60779;  
 XX  
 DT 20-JUL-1999 (first entry)

XX  
 DE soybean cytochrome P450 enzyme, CYP93C1 encoding cDNA.  
 XX  
 KW Soybean; Solanaceae crop plant; cytochrome P450; transgenic plant;  
 KW enzyme; phenylurea herbicide; herbicide resistance; ss.  
 XX  
 OS Glycine max.  
 XX  
 FN W0919493-A2.  
 XX  
 PD 22-APR-1999.  
 XX  
 PF 05-OCT-1998; 98MO-US20807.  
 XX  
 PR 10-OCT-1997; 97US-0948564.  
 XX  
 PA (UNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 PI Corbin FT, Dewey RE, Siminszky B;  
 XX  
 DR WP1; 1999-302532/25.  
 DR P-PSDB; AAY09189.  
 XX  
 PT DNA encoding soybean cytochrome P450 enzymes  
 XX  
 PS Claim 1; Page 66-69; 93pp; English.  
 CC The invention provides new DNA molecules (AAX60773-X60781) encoding  
 CC soybean cytochrome P450 enzymes (AAY09183-X09191) respectively. The DNA  
 CC encoding the cytochrome P450 enzymes is useful for transformation of  
 CC Solanaceae crop plants. Transgenic plants comprising DNA constructs  
 CC having the P450 encoding nucleic acid sequences are resistant to  
 CC phenylurea herbicides. The transgenic plants have increased resistance to  
 CC phenylurea herbicides compared to wild-type plants of the same species.  
 CC The plant crops, e.g. turfgrass, tobacco, potato, tomato, corn, rice,  
 CC cotton, soybean, rape, wheat, oats, barley or rice are particularly  
 CC resistant to fluometuron, linuron, chlorthaluron or diuron.  
 XX  
 SQ Sequence 1824 BP; 497 A; 448 C; 416 G; 463 T; 0 other.  
 Alignment Scores:  
 Pred. No.: 4,01e-270 Length: 1824  
 Score: 2251.00 Matches: 451  
 Percent Similarity: 86.76% Conservative: 1  
 Best Local Similarity: 86.56% Mismatches: 69  
 Query Match: 93.95% Indels: 0  
 DB: 20 Gaps: 0  
 US-09-857-581-66 (1-521) x AAX60779 (1-1824).  
 QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu\*\*\*ValLeuAlaLeuPhe\*\*\*HisLeuArgPro 20  
 Db 54 ATGTGCTTGACACTTGCATCTGGTGTATGTGCTGTGTGCTGTGACCTGCGGCC 113  
 QY 21 ThrPro\*\*\*Ala\*\*\*SerIysAlaLeuArgHisLeuProAsnProSerPro\*\*\*Pro 40  
 Db 114 ACACCACTGCAAAATCAAGACACTTGCATCTTCCAAACCAACCAAGGCTT 173

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 102e  
 date 10/10/97

QY 41 ArgLeuProHleGlyHis\*\*\*HisLeuLeuysAspLysLeuLeuHisTyrAla\*\*\* 60  
 DB 174 CGCTCTCCCTTCATGACACCTTCAATTAAGACAACTTCTCCATCGACATC 233  
 QY 61 IleAspLeuSerLysHisGlyProLeuPheSer\*\*\*\*\*PheGlySerMetProThr 80  
 DB 234 ATGACCTCTCAAAAACATGATGCTTATCTCTCTACTCTGCTCATGACCAACC 293  
 QY 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln\*\*\*\*\*GluAlaThrSer 100  
 DB 294 GTTGTGCTCCACACACAGATTTCTCAAGCTTCTCTCCAAACGACAGGACATTC 353  
 QY 101 Phe\*\*\*ThrArgPheGlnThrSerAla\*\*\*Arg\*\*\*LeuThrTyrAsp\*\*\*\*\*ValAla 120  
 DB 354 TTCAACCAAGTTCACAACTCCAGCCATTAAGAGCTCAGCTATGATAGTCAGTGGCC 413  
 QY 121 \*\*\*\*\*Pro\*\*\*GlyProTyrTrp\*\*\*PheValArgLysLeuLeuMetAsnAspLeu 140  
 DB 414 ATGCTTCCCTTCGACCTTACTGAGAGTTCGTGAGAGGATCATCATGACACTTCC 473  
 QY 141 AsnAlaThrThrValAsn\*\*\*LeuArgProLeuArgThrGlnIleArgLys\*\*\*Leu 160  
 DB 474 AAGCGACACCTGTAAACAGTTGAGGCTTTGAGAGCCACACACCGGACAGTCTT 533  
 QY 161 Arg\*\*\*MetAlaGln\*\*\*AlaGluAla\*\*\*LysProLeuAsp\*\*\*ThrGluLeuLeu 180  
 DB 534 AGGTTTGCCCAAGGCGGACAGGACAGAAAGCCCTTACCTACACAGAGCTTCTG 593  
 QY 181 LysTrp\*\*\*AsnSerThr\*\*\*SerMetMet\*\*\*LeuGlyGluAlaGluIleArgAsp 200  
 DB 594 AATATGACCAACAGCATCTCATGATGATGCTCGGCGAGGCTGAGAGATCAGAGC 653  
 QY 201 IleAlaArgLysValLeuLysIle\*\*\*GlyGluTyrSerLeuThrAspPheIle\*\*\*Pro 220  
 DB 654 ATCGCTGCGAGGTTCTTAAGATCTTGGCAATACAGCTCATGACTTCACTCTGCCA 713  
 QY 221 LeuLys\*\*\*LeuLysValGlyTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240  
 DB 714 TTGAGCATCTCAAGGTTGAAAGTATGAGAGAGATGACAGCATCTTGAACAAGTTC 773  
 QY 241 AspProValValGluArgValIleLysLysArgArg\*\*\*IleValArgArgArg\*\*\*Asn 260  
 DB 774 GACCTGTCTGTAAGGCTCATCAAGAGCGCGTGAATGCTGAGAGAGAGAAAGAAC 833  
 QY 261 GlyLys\*\*\*\*\*GluGlyGlu\*\*\*SerGlyVal\*\*\*LeuAspThrLeuLeuGluPheAla 280  
 DB 834 GGAGAGGTTGTGAGGCTGAGGCTCAGCGGGGTTTCTTGACACTTGTGAATTCGCT 893  
 QY 281 GluAspGluThr\*\*\*GluIleLysIleThrLys\*\*\*\*\*IleLysGlyLeuValValAsp 300  
 DB 894 GAGCATGAGCATGAGATCAAAATCAACAGACCAACATGAGAGGCTTGTGTGAC 953  
 QY 301 \*\*\*PheSerAlaGly\*\*\*AspSerThrAla\*\*\*\*\*ThrGluTrpAlaLeuAlaGluLeu 320  
 DB 954 TTTTCTCGGACGAAACGACTCTCAAGCGGTGGCAACAGAGTGGCATTTGGCAAGACTC 1013

QY 321 IleAsnAspPro\*\*\*ValLeu\*\*\*\*\*AlaArgGluLys\*\*\*TyrSerValValGlyLys 340  
 DB 1014 ATCAACAATCTTGAAGTGTGAAAAGGCTCTGAGAGGCTCTCAAGTGTGGGAAAG 1073  
 QY 341 Asp\*\*\*LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360  
 DB 1074 GACAGACTTGTGACAGAGATTGACACTCAAAACCTTCTTACATTAGAGCAATCGAAG 1133  
 QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys\*\*\*GluGlyCys 380  
 DB 1134 GAGCATTCGCGATGACCCGACCTCCAGATGTGCAAAAGAAATGACAGAAAGTGT 1193  
 QY 381 \*\*\*IleAsnGly\*\*\*Val\*\*\*ProGluGlyAlaLeu\*\*\*\*\*PheAsnValTrpGlnVal 400  
 DB 1194 GAGATTATGATATGATGATCCAGAGAGGATTTCTCTCAATGATATGAGCAAGTA 1253  
 QY 401 Gly\*\*\*Asp\*\*\*LysTyrTrpAspArgProSerGlu\*\*\*ArgProGluArgPheLeuGlu 420  
 DB 1254 GGAAGAGACCCCAAAATATGAGGACACACATCGAGTTCGTCGAGAGGTTCTTAG 1313  
 QY 421 Thr\*\*\*AlaGluGlyGluAla\*\*\*\*\*LeuAspLeuArgGly\*\*\*HisPheGlnLeuLeu 440  
 DB 1314 ACGAGGCTGTGAAGGAGAGACAGGCGCTTATCTTGAAGGACACATTTCAACTTCTC 1373  
 QY 441 PropheGlySerGlyArg\*\*\*MetCysProGlyVal\*\*\*LeuAlaThrSerGly\*\*\*Ala 460  
 DB 1374 CCATTGGGCTGTGAGAGAGATGTGCTCGAGATCAATGTGCTACTTGGAGATGGCA 1433  
 QY 461 ThrLeuLeuAlaSerLeuLeuGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480  
 DB 1434 ACACCTTCTCATCTTATTAATGATGCTTGCATGCAATGCTGGGCTGCAACAGACAG 1493  
 QY 481 IleLeuLysGly\*\*\*AspAlaLysValSerMetGluLysArgAlaGlyLeuThrValPro 500  
 DB 1494 ATATTGAAGGCTGTACGCCAAAGTTACATGAGAGAGAGCGGCTCATCTGTCCA 1553  
 QY 501 ArgAlaHisSerLeuValCysValProLeuAlaArgGlyValAlaLysLysLeuLeu 520  
 DB 1554 AGGACACATAGTCTTGTCTGTGTTCACCTTGCAAGATCGGCGTTCATTAACCTCTT 1613  
 QY 521 Ser 521  
 DB 1614 TCT 1616

RESULT 11  
 AAA72444  
 ID AAA72444 standard; cDNA, 1824 BP.  
 XX  
 AC AAA72444;  
 XX  
 DT 19-DEC-2000 (first entry)  
 XX  
 DE Soybean CYP93C1 isoflavone synthase cDNA.  
 KW Soybean; CYP93C1; cytochrome P450; isoflavone synthase;  
 isoflavonoid biosynthesis; phenylpropanoid pathway; leguminous plant;  
 defence response; attractant; repellent; signal compound; antibiotic;

